AMENDMENTS TO THE SPECIFICATION

Please delete the sequence listing previously submitted on compact disc in the preliminary amendment and replace with the sequence listing submitted on compact disc enclosed herewith.

In the specification at page 1, after the section entitled "RELATED APPLICATIONS" inserted in the preliminary amendment, please replace the section entitled "SUBMISSION ON COMPACT DISC" with the following amended paragraph:

SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2) and a computer readable form copy of the Sequence Listing (CRF COPY), all on compact disc , each containing: file name: Sequence List-13477-00002-US, date recorded: October 24, 2007, size: 168 KB.

In the specification at page 6, line 4, please replace the paragraph which starts with "Thus, the term "reference" relates" with the following amended paragraph:

Thus, the term "reference" relates for example to an organism or a part thereof, e.g. a cell, which is essentially genetically, proteomically, and/or metabolically identical to the organism of the present invention or a part thereof but an activity of a specific gene product, e.g. Rpi-blb2, cannot be observed as there is a relevant difference in the reference's genome, proteome or metabolome. Thus, the reference can be a plant or a part thereof which does not express or expresses too little of a relevant active gene product, e.g. it does not encode a Rpi-blb2 or does not transcribe a Rpi-blb2 encoding gene or does not translate an active Rpi-blb2 mRNA . Thus, the reference does not provide the modification creating an active gene product in a sufficient quantity to result in an phenotype as described.[[.]] Whether two plants are essentially genetically identical can be tested with assays known to a person skilled in the art, e.g. via fingerprint analysis, e.g. as described in Roldan-Ruiz, Theor. Appl. Genet., 2001, 1138-1150. The expression pattern of proteins can be tested as described in the art e.g. via gel electrophoresis (1D, 2D, 3D), mass spectrometric analysis and other methods ~~as described for example in www.waters.com, www.proteine.org.au, www.proteomesci.com,~~

~~www.sdu.dk/Nat/CPA~~. The metabolome can be analysed by the skilled as described in the art, e.g. via HPLC, GC, OPLC, LC-MS, GC-MS, LC-MS-MS, and other methods as described e.g. in ~~www.metabolic-explorer.com, www.ki.se/icsb2002/pdf/ICSB_209.pdf, www.genomics.rug.nl/technologies.htm,~~ Fiehn et al., Nature Biotech, 18 (2000), 1157, Raamsdonk et al., Nature Biotech, 19 (2991), 45-50, Buchholz, Anal. Biochem, 295 (2001) 129-137, Soga et al., Anal Chem. 74 (2002) 2233-2239.

In the specification at page 19, line 27, please replace the paragraph which starts with "In the present application" with the following amended paragraph:

In the present application, the homology was determined with the program clustalW ~~which can be found on www.ebi.ac.uk/tools~~, choose sequence analyses and choose option clustalW (multiple sequence alignments). All options were performed under standard conditions, as follows:

In the specification at page 71, line 4, please replace the paragraph which starts with "These and other embodiments" with the following amended paragraph:

These and other embodiments are disclosed and encompassed by the description and examples of the present invention. Further literature concerning any one of the methods, uses and compounds to be employed in accordance with the present invention may be retrieved from public libraries, using for example electronic devices. For example the public database "Medline" may be utilized which is available on the Internet~~, for example under http://www.ncbi.nlm.nih.gov/PubMed/medline.html~~. Further databases and addresses~~, such as http://www.ncbi.nlm.nih.gov/, http://www.infobiogen.fr/, http://www.fmi.ch/biology/research-tools.html, http://www.tigr.org/,~~ are known to the person skilled in the art and can also be obtained ~~using, e.g., http://www.lycos.com~~. An overview of patent information in biotechnology and a survey of relevant sources of patent information useful for retrospective searching and for current awareness is given in Berks, TIBTECH 12 (1994), 352-364.

In the specification at page 92, line 26, please replace the paragraph which starts with "The deduced open reading frame" with the following amended paragraph:

The deduced open reading frame of the Rpi-blb2 gene encodes a predicted polypeptide of 1267 amino acids with an estimated molecular weight of 146 kD (Figure 14). Several functional motifs present in R genes of the NBS-LRR class of plant R genes are apparent in the encoded protein. As illustrated in Figure 14, the Rpi-blb2 protein belongs to the leucine zipper (LZ) subset of NBS-LRR resistance proteins. The N-terminal half of the Rpi-blb2 protein contains a potential LZ region between amino acids 413 and 434 and six conserved motifs indicative of a nucleotide-binding site (van der Biezen and Jones, 1998). The C-terminal half of Rpi-blb comprises a series of 15 irregular LRRs that can be aligned according to the consensus sequence ~~hxxhxxLxxLxLxxC/N/Sx(x)LxxLPxx~~ hxxhxxLxxLxLxxC/N/SxLxxLPxx (SEQ ID NO: 100) or hxxhxxLxxLxLxxC/N/SxxLxxLPxx (SEQ ID NO: 101) observed in other cytoplasmic R proteins, whereby h can be L, I, M, V or F, and x any amino acid residue (Jones and Jones, 1997).